

What is claimed is:

1. A microorganism which is deficient in
repressor of L-methionine biosynthesis system and has L-
5 methionine productivity.

2. A microorganism having enhanced
intracellular homoserine transsuccinylase activity and
L-methionine productivity.

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3. A microorganism which is deficient in
repressor of L-methionine biosynthesis system, and has
enhanced intracellular homoserine transsuccinylase
activity and L-methionine productivity.

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4. The microorganism according to any one of
claims 1 to 3, which further exhibits reduced
intracellular S-adenosylmethionine synthetase activity.

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ENOC 5. The microorganism according to any one of
claims 2 to 4, wherein the enhanced homoserine
transsuccinylase activity is obtained by increasing copy
number of a gene coding for the intracellular homoserine
transsuccinylase, or enhancing an expression regulatory
25 sequence for the gene.

ENOC 6. The microorganism according to claim 1 or 4,

which has homoserine transsuccinylase for which concerted inhibition by L-methionine and S-adenosylmethionine is desensitized.

TMDC 5. The microorganism according to any one of claims 1 to 6, which exhibits L-threonine auxotrophy.

TMDC 8. The microorganism according to any one of claims 1 to 7, which exhibits enhanced intracellular 10 cystathione γ -synthase activity and enhanced intracellular aspartokinase-homoserine dehydrogenase II activity.

TMDC 9. The microorganism according to any one of 15 claims 1 to 8, which belongs to the genus *Escherichia*.

TMDC 10. A method for producing L-methionine which comprises culturing the microorganism according to any one of claims 1 to 9 in a medium to produce and 20 accumulate L-methionine in the medium, and collecting the L-arginine from the medium.

11. A DNA which codes for homoserine transsuccinylase for which concerted inhibition by L-methionine and S-adenosylmethionine is desensitized, 25 wherein the homoserine transsuccinylase has the amino acid sequence of SEQ ID NO: 26 including a mutation

corresponding to replacement of arginine by cysteine at
the 27th position, mutation corresponding to replacement
of isoleucine by serine at the 296th position, mutation
corresponding to replacement of proline by leucine at
5 the 298th position, mutation corresponding to
replacement of arginie by cysteine at the 27th position
and replacement of isoleucine by serine at the 296th
position, mutation corresponding to replacement of
isoleucine by serine at the 296th position and
10 replacement of proline by leucine at the 298th position,
mutation corresponding to replacement of proline by
leucine at the 298th position and replacement of
arginine by cysteine at the 27th position, or mutation
corresponding to replacement of arginine by cysteine at
15 the 27th position, replacement of isoleucine by serine
at the 296th position and replacement of proline by
leucine at the 298th position.